

NEL-0001 Sequence Listing.txt SEQUENCE LISTING

<110> The Minister of National Defence, Government of Canada Nagata, Leslie P Wong, Jonathon P
<120> Novel DNA-Based Vaccine Against the Encephalitis Alphaviruses
<130> NEL-001
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<150> 60/256,948 <151> 2000-12-21
<160> 7
<170> PatentIn version 3.1
<210> 1 <211> 11484 <212> DNA <213> Western equine encephalomyelitis virus - strain 71V-1658
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Tyr	Leu	Gln	Pro	Glu 2040	Ile				Seque Val 2045					G]n 2050	
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									ray	C 11					

		gct Ala 2505													7625
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65 70 75 80 Ile Cys Pro Met Ile Ser Ala Glu Asp Pro Asp Arg Leu Gln Arg Tyr Ala Glu Arg Leu Lys Lys Ser Asp Ile Thr Asp Lys Asn Ile Ala Ser 100 105 110 Lys Ala Ala Asp Leu Leu Glu Val Met Ser Thr Pro Asp Ala Glu Thr 115 120 125 115 Pro Ser Leu Cys Met His Thr Asp Ala Thr Cys Arg Tyr Phe Gly Ser 130 135 140 Val Ala Val Tyr Gln Asp Val Tyr Ala Val His Ala Pro Thr Ser Ile

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145 Tyr His Gln Ala Leu Lys Gly Val Arg Thr Ile Tyr Trp Ile Gly Phe 165 170 175 Asp Thr Thr Pro Phe Met Tyr Lys Asn Met Ala Gly Ser Tyr Pro Thr 180 185 190 Tyr Asn Thr Asn Trp Ala Asp Glu Arg Val Leu Glu Ala Arg Asn Ile 195 200 205 Gly Leu Gly Asn Ser Asp Leu Gln Glu Ser Arg Leu Gly Lys Leu Ser 210 220 Ile Leu Arg Lys Lys Arg Leu Gln Pro Thr Asn Lys Ile Ile Phe Ser 235 230 235 Val Gly Ser Thr Ile Tyr Thr Glu Asp Arg Ser Leu Leu Arg Ser Trp 245 250 255 His Leu Pro Asn Val Phe His Leu Lys Gly Lys Ser Asn Phe Thr Gly 260 265 270 Arg Cys Gly Thr Ile Val Ser Cys Glu Gly Tyr Val Ile Lys Lys Ile 275 280 285 Thr Ile Ser Pro Gly Leu Tyr Gly Lys Val Glu Asn Leu Ala Ser Thr 290 295 300 Met His Arg Glu Gly Phe Leu Ser Cys Lys Val Thr Asp Thr Leu Arg 305 310 315 320 305 Gly Glu Arg Val Ser Phe Ala Val Cys Thr Tyr Val Pro Ala Thr Leu 325 330 335 Cys Asp Gln Met Thr Gly Ile Leu Ala Thr Asp Val Ser Val Asp Asp 340 345 350 Ala Gln Lys Leu Leu Val Gly Leu Asn Gln Arg Ile Val Val Asn Gly 355 360 365 Arg Thr Gln Arg Asn Thr Asn Thr Met Gln Asn Tyr Leu Leu Pro Val

Val Ala Gln Ala Phe Ser Arg Trp Ala Arg Glu His Arg Ala Asp Leu

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Lys Thr Gln Asp Thr Asp Ser Glu Tyr Val Phe Asp Ile Asp Ala Arg 660 665 670 Lys Cys Val Lys Arg Glu Asp Ala Gly Pro Leu Cys Leu Thr Gly Asp 675 680 685 Leu Val Asp Pro Pro Phe His Glu Phe Ala Tyr Glu Ser Leu Lys Thr 690 695 700 Arg Pro Ala Ala Pro His Lys Val Pro Thr Ile Gly Val Tyr Gly Val 705 710 715 720 Pro Gly Ser Gly Lys Ser Gly Ile Ile Lys Ser Ala Val Thr Lys Lys
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- Ala Ser Gln Gly Leu Thr Arg Lys Gly Val Tyr Ala Val Arg Tyr Lys 915 920 925
- Val Asn Glu Asn Pro Leu Tyr Ser Gln Thr Ser Glu His Val Asn Val 930 940
- Leu Leu Thr Arg Thr Glu Lys Arg Ile Val Trp Lys Thr Leu Ala Gly 945 950 955 960
- Asp Pro Trp Ile Lys Thr Leu Thr Ala Lys Tyr Pro Gly Asp Phe Thr 965 970 975
- Ala Ser Leu Asp Asp Trp Gln Arg Glu His Asp Ala Ile Met Ala Arg 980 985 990
- Val Leu Asp Lys Pro Gln Thr Ala Asp Val Phe Gln Asn Lys Val Asn 995 1000 1005
- Val Cys Trp Ala Lys Ala Leu Glu Pro Val Leu Ala Thr Ala Asn 1010 1015 1020
- Ile Val Leu Thr Arg Gln Gln Trp Glu Thr Leu His Pro Phe Lys 1025 1030 1035
- His Asp Arg Ala Tyr Ser Pro Glu Met Ala Leu Asn Phe Phe Cys 1040 1045 1050
- Thr Arg Phe Phe Gly Val Asp Leu Asp Ser Gly Leu Phe Ser Ala 1055 1060 1065
- Pro Thr Val Ala Leu Thr Tyr Arg Asp Gln His Trp Asp Asn Ser 1070 1075 1080
- Pro Gly Lys Asn Met Tyr Gly Leu Asn Arg Glu Val Ala Lys Glu 1085 1090 1095
- Leu Ser Arg Arg Tyr Pro Cys Ile Thr Lys Ala Val Asp Thr Gly 1100 1110
- Arg Val Ala Asp Ile Arg Asn Asn Thr Ile Lys Asp Tyr Ser Pro 1115 1120 1125
- Thr Ile Asn Val Val Pro Leu Asn Arg Arg Leu Pro His Ser Leu 1130 1140
- Ile Val Asp His Lys Gly Gln Gly Thr Thr Asp His Ser Gly Phe Page 21

	1145					1150	L-00	01 S	eque	nce	1155 1155	ng.t	xt	
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Ile	Ser 1175	Ile	Pro	Gly	Lys	Lys 1180	val	Glu	Ser	Met	Gly 1185	Pro	Leu	Pro
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Asn	Ile 1265	Ile	Thr	Ala	val	Ala 1270	Arg	Ser	Phe	Arg	Phe 1275	Thr	Arg	val
Cys	Gln 1280		Lys	Asn	Thr	А]а 1285	Glu	Asn	Thr	Glu	val 1290	Leu	Phe	val
Phe	Phe 1295	Gly	Lys	Asp	Asn	Gly 1300	Asn	ніѕ	Thr	His	Asp 1305	Gln	Asp	Arg
Leu	Gly 1310	val	val	Leu	Asp	Asn 1315	Ile	Tyr	Gln	Gly	Ser 1320	Thr	Arg	Tyr
Glu	Ala 1325	Gly	Arg	Ala	Pro	Ala 1330	Tyr	Arg	val	Ile	Arg 1335	Gly	Asp	Ile
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Phe	Ser 1400	Lys	Met	Pro	Glu	Pro 1405	Glu	Gly	Asp	Leu	Lys 1410	Leu	Ala	Аlа
Αla	Tyr 1415	Met	Ser	Ile	Ala	Ser 1420		val	Asn	Ala	Glu 1425	Arg	Ile	Thr
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Lys	Asp 1445	Arg	val	Met	Gln	Ser 1450	Leu	нis	ніѕ	Leu	Phe 1455	Thr	Ala	Phe
Asp	Thr 1460		Asp	Ala	Asp	Val 1465	Thr	Ile	Tyr	Cys	Leu 1470	Asp	Lys	Gln
Тгр	Glu 1475	Thr	Àrg	Ile	Ile.	Glu 1480	Ala	Ile	His	Arg	Lys 1485	Glu	Ser	٧al
Glu	Ile 1490	Leu	Asp	Asp	Asp	Lys 1495	Pro	∨al	Asp	Ile	Asp 1500	Leu	٧a٦	Arg
Val	ніs 1505	Pro	Asn	Ser	Ser	Leu 1510		Gly	Arg	Pro	Gly 1515	Tyr	Ser	val
Asn	Glu 1520	Gly	Lys	Leu	Tyr	Ser 1525	Tyr	Leu	Glu	Gly	Thr 1530	Arg	Phe	His
Gln	Thr 1535	Ala	Lys	Asp	Ile	Ala 1540	Glu	Ile	His	Ala	Met 1545	Trp	Pro	Asn
Lys	Ser 1550	Glu	Ala	Asn	Glu	G]n 1555	Ile	Cys	Leu	Tyr	Ile 1560	Leu	Glу	Glu
Ser	Met 1565	Ser	Ser	Ile	Arg	Ser 1570	Lys	Cys	Pro	val	Glu 1575	Glu	Ser	Glu
Ala	Ser 1580	Ala	Pro	Pro	His	Thr 1585	Leu	Pro	Cys	Leu	Cys 1590	Asn	Tyr	Ala
Met	Thr 1595	Ala	Glu	Arg	Val	туг 1600	Arg	Leu	Arg	Ser	Ala 1605	Lys	Lys	Glu
Gln	Phe 1610	Аlа	val	Cys	Ser	Ser 1615	Phe	Leu	Leu	Pro	Lys 1620	Tyr	Arg	Ile

Thr Gly Val Gln Lys Leu Gln Cys Ser Lys Pro Val Leu Phe Ser Gly Val Val Pro Pro Ala Val His Pro Arg Lys Tyr Ala Glu Ile 1640 1650 1640 Ile Leu Glu Thr Pro Pro Pro Ala Thr Thr Val Ile Cys 1660 Glu Pro Thr Val Pro Glu Arg Ile Pro Ser Pro Val Ile Ser Arg 1670 1680 Ala Pro Ser Ala Glu Ser Leu Leu Ser Leu Gly Gly Val Ser Phe Ser Ser Ser Ala Thr Arg Ser Ser Thr Ala Trp Ser Asp Tyr Asp 1700 1705 1710 Arg Arg Phe Val Val Thr Ala Asp Val His Gln Ala Asn Thr Ser Thr Trp Ser Ile Pro Ser Ala Pro Gly Leu Asp Val Gln Leu Pro Ser Asp Val Thr Asp Ser His Trp Ser Ile Pro Ser Ala Ser Gly 1745 1750 1755 Phe Glu Val Arg Thr Pro Ser Val Gln Asp Leu Thr Ala Glu Cys 1760 Ala Lys Pro Arg Gly Leu Ala Glu Ile Met Gln Asp Phe Asn Thr 1775 1780 1785 Ala Pro Phe Gln Phe Leu Ser Asp Tyr Arg Pro Val Pro Ala Pro Arg Arg Arg Pro Ile Pro Ser Pro Arg Ser Thr Ala Ser Ala Pro 1805 1810 1815 Pro Val Pro Lys Pro Arg Arg Thr Lys Tyr Gln Gln Pro Pro Gly 1820 1830 Val Ala Arg Ala Ile Ser Glu Ala Glu Leu Asp Glu Tyr Ile Arg Gln His Ser Asn 1850

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Asp Ser Ala Ala Phe Asn Val Asp Cys Phe Lys Lys Tyr Ala Cys Asn 225 230 235 240 Asp Glu Tyr Trp Asp Thr Phe Arg Asp Asn Pro Ile Arg Leu Thr Thr 245 250 255 Glu Asn Val Thr Gln Tyr Val Thr Lys Leu Lys Gly Pro Lys Ala Ala 260 265 270 Ala Leu Phe Ala Asn Thr His Asn Leu Lys Pro Leu Gln Glu Ile Pro 275 280 285 Met Asp Gln Phe Val Met Asp Leu Lys Arg Asp Val Lys Val Thr Pro 290 295 300 Gly Thr Lys His Thr Glu Glu Arg Pro Lys Val Gln Val Ile Gln Ala 305 310 315 320 Ala Asp Pro Leu Ala Thr Ala Tyr Leu Cys Gly Ile His Arg Glu Leu 325 330 335 Val Arg Arg Leu Asn Ala Val Leu Leu Pro Asn Ile His Thr Leu Phe 340 345 350 Asp Met Ser Ala Glu Asp Phe Asp Ala Ile Ile Ala Glu His Phe His 355 360 365 His Gly Asp Pro Val Leu Glu Thr Asp Ile Ala Ser Phe Asp Lys Ser 370 380 Glu Asp Asp Ala Ile Ala Ile Ser Ala Leu Met Ile Leu Glu Asp Leu 385 390 395 400 Gly Val Asp Gln Pro Leu Leu Asp Leu Ile Glu Ala Ala Phe Gly Asn 405 410 415 Ile Thr Ser Val His Leu Pro Thr Gly Thr Arg Phe Lys Phe Gly Ala 420 430 Met Met Lys Ser Gly Met Phe Leu Thr Leu Phe Val Asn Thr Leu Val 435 440 445 Asn Ile Met Ile Ala Ser Arg Val Leu Arg Glu Arg Leu Thr Thr Ser 450 455 460 Ala Cys Ala Ala Ser Ile Gly Asp Asp Asn Ile Val His Gly Val Val Page 26

Ser Asp Thr Leu Met Ala Glu Arg Cys Ala Thr Trp Leu Asn Met Glu

Val Lys Ile Ile Asp Ala Val Ile Gly Ile Lys Ala Pro Tyr Phe Cys 500 510

Gly Gly Phe Ile Leu Val Asp Gln Ile Thr Gly Thr Ala Cys Arg Val 515 520 525

Ala Asp Pro Leu Lys Arg Leu Phe Lys Leu Gly Lys Pro Leu Pro Val 530 540

Asp Asp Thr Gln Asp Cys Asp Arg Arg Arg Ala Leu His Asp Glu Ala 545 550 555 560

Met Arg Trp Asn Arg Ile Gly Ile Thr Asp Glu Leu Val Lys Ala Val 565 570 575

Glu Ser Arg Tyr Glu Ile Ile Leu Ala Gly Leu Ile Ile Thr Ser Leu 580 585 590

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PRT

Western equine encephalomyelitis virus - strain 71v-1658 <400>

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Val Asn Leu Thr Phe Lys Gln Arg Ser Pro Asn Pro Pro Gly Pro 50 60

Pro Pro Lys Lys Lys Ser Ala Pro Lys Pro Lys Pro Thr Gln Pro Page 27

65

Lys Lys Lys Gln Gln Ala Lys Arg Thr Lys Arg Lys Pro Lys Pro 85 90 95 Gly Lys Arg Gln Arg Met Cys Met Lys Leu Glu Ser Asp Lys Thr Phe $100 \hspace{1cm} 105 \hspace{1cm} 110$ Pro Ile Met Leu Asn Gly Gln Val Asn Gly Tyr Ala Cys Val Val Gly 115 120 125 Gly Arg Leu Met Lys Pro Leu His Val Glu Gly Lys Ile Asp Asn Glu 130 135 140 Gln Leu Ala Ala Val Lys Leu Lys Lys Ala Ser Met Tyr Asp Leu Glu 145 150 155 160 Tyr Gly Asp Val Pro Gln Asn Met Lys Ser Asp Thr Leu Gln Tyr Thr 165 170 175 Ser Asp Lys Pro Pro Gly Phe Tyr Asn Trp His His Gly Ala Val Gln Tyr Glu Asn Gly Arg Phe Thr Val Pro Arg Gly Val Gly Gly Lys Gly 195 200 205 Asp Ser Gly Arg Pro Ile Leu Asp Asn Arg Gly Arg Val Val Ala Ile 210 215 220 Val Leu Gly Gly Ala Asn Glu Gly Thr Arg Thr Ala Leu Ser Val Val 225 230 235 240 Thr Trp Asn Gln Lys Gly Val Thr Ile Arg Asp Thr Pro Glu Gly Ser 245 250 255 Glu Pro Trp Ser Leu Val Thr Ala Leu Cys Val Leu Ser Asn Val Thr 260 265 270 Phe Pro Cys Asp Lys Pro Pro Val Cys Tyr Ser Leu Thr Pro Glu Arg 275 280 285 Thr Leu Asp Val Leu Glu Glu Asn Val Asp Asn Pro Asn Tyr Asp Thr 290 295 300 Leu Leu Glu Asn Val Leu Lys Cys Pro Ser Arg Arg Pro Lys Arg Ser 305 310 315 320

NEL-0001 Sequence Listing.txt Ile Thr Asp Asp Phe Thr Leu Thr Ser Pro Tyr Leu Gly Phe Cys Pro 325 330 335 Tyr Cys Arg His Ser Thr Pro Cys Phe Ser Pro Ile Lys Ile Glu Asn 340 345 350 Val Trp Asp Glu Ser Asp Asp Gly Ser Ile Arg Ile Gln Val Ser Ala 355 360 365 Gln Phe Gly Tyr Asn Gln Ala Gly Thr Ala Asp Val Thr Lys Phe Arg 370 375 380 Tyr Met Ser Phe Asp His Asp His Asp Ile Lys Glu Asp Ser Met Glu 385 390 395 400 Lys Ile Ala Ile Ser Thr Ser Gly Pro Cys Arg Arg Leu Gly His Lys 405 410 415Gly Tyr Phe Leu Leu Ala Gln Cys Pro Pro Gly Asp Ser Val Thr Val 420 425 430 420 Ser Ile Thr Ser Gly Ala Ser Glu Asn Ser Cys Thr Val Glu Lys Lys 435 440 445 Ile Arg Arg Lys Phe Val Gly Arg Glu Glu Tyr Leu Phe Pro Pro Val 450 460 His Gly Lys Leu Val Lys Cys His Val Tyr Asp His Leu Lys Glu Thr 465 470 475 480 Ser Ala Gly Tyr Ile Thr Met His Arg Pro Gly Pro His Ala Tyr Lys 485 490 495 Ser Tyr Leu Glu Glu Ala Ser Gly Glu Val Tyr Ile Lys Pro Pro Ser 500 505 510 Gly Lys Asn Val Thr Tyr Glu Cys Lys Cys Gly Asp Tyr Ser Thr Gly 515 520 525 Ile Val Ser Thr Arg Thr Lys Met Asn Gly Cys Thr Lys Ala Lys Gln 530 540 Cys Ile Ala Tyr Lys Ser Asp Gln Thr Lys Trp Val Phe Asn Ser Pro 545 550 555 560 Asp Leu Ile Arg His Thr Asp His Ser Val Gln Gly Lys Leu His Ile 565 570 575

Pro Phe Arg Leu Thr Pro Thr Val Cys Pro Val Pro Leu Ala His Thr 580 585 590 Pro Thr Val Thr Lys Trp Phe Lys Gly Ile Thr Leu His Leu Thr Ala 595 600 605 Met Arg Pro Thr Leu Leu Thr Thr Arg Lys Leu Gly Leu Arg Ala Asp 610 615 620 Ala Thr Ala Glu Trp Ile Thr Gly Ser Thr Ser Arg Asn Phe Ser Val 625 635 640 Gly Arg Glu Gly Leu Glu Tyr Val Trp Gly Asn His Glu Pro Val Arg 645 650 655 Val Trp Ala Gln Glu Ser Ala Pro Gly Asp Pro His Gly Trp Pro His 660 665 670 Glu Ile Ile His Tyr Tyr His Arg His Pro Val Tyr Thr Val Ile 675 680 685 Val Leu Cys Gly Val Ala Leu Ala Ile Leu Val Gly Thr Ala Ser Ser 690 695 700 Ala Ala Cys Ile Ala Lys Ala Arg Arg Asp Cys Leu Thr Pro Tyr Ala 705 710 715 720 Leu Ala Pro Asn Ala Thr Val Pro Thr Ala Leu Ala Val Leu Cys Cys
725
730
735 Ile Arg Pro Thr Asn Ala Glu Thr Phe Gly Glu Thr Leu Asn His Leu 740 745 750 Trp Phe Asn Asn Gln Pro Phe Leu Trp Ala Gln Leu Cys Ile Pro Leu 755 760 765 Ala Ala Leu Val Ile Leu Phe Arg Cys Phe Ser Cys Cys Met Pro Phe 770 780 Leu Leu Val Ala Gly Val Cys Leu Gly Lys Val Asp Ala Phe Glu His 785 790 795 800 Ala Thr Thr Val Pro Asn Val Pro Gly Ile Pro Tyr Lys Ala Leu Val 805 810 815 Glu Arg Ala Gly Tyr Ala Pro Leu Asn Leu Glu Ile Thr Val Val Ser 820 825 830 Page 30

- Ser Glu Leu Thr Pro Ser Thr Asn Lys Glu Tyr Val Thr Cys Lys Phe 835 840 845
- His Thr Val Ile Pro Ser Pro Gln Val Lys Cys Cys Gly Ser Leu Glu 850 855 860
- Cys Lys Ala Ser Ser Lys Ala Asp Tyr Thr Cys Arg Val Phe Gly Gly 865 870 875 880
- Val Tyr Pro Phe Met Trp Gly Gly Ala Gln Cys Phe Cys Asp Ser Glu 885 890 895
- Asn Thr Gln Leu Ser Glu Ala Tyr Val Glu Phe Ala Pro Asp Cys Thr 900 905 910
- Ile Asp His Ala Val Ala Leu Lys Val His Thr Ala Ala Leu Lys Val 915 920 925
- Gly Leu Arg Ile Val Tyr Gly Asn Thr Thr Ala His Leu Asp Thr Phe 930 935 940
- Val Asn Gly Val Thr Pro Gly Ser Ser Arg Asp Leu Lys Val Ile Ala 945 950 955 960
- Gly Pro Ile Ser Ala Ala Phe Ser Pro Phe Asp His Lys Val Val Ile 965 970 975
- Arg Lys Gly Leu Val Tyr Asn Tyr Asp Phe Pro Glu Tyr Gly Ala Met 980 985 990
- Lys Pro Gly Ala Phe Gly Asp Ile Gln Ala Ser Ser Leu Asp Ala Thr 995 1000 1005
- Asp Ile Val Ala Arg Thr Asp Ile Arg Leu Leu Lys Pro Ser Val 1010 1015 1020
- Lys Asn Ile His Val Pro Tyr Thr Gln Ala Val Ser Gly Tyr Glu 1025 1030 1035
- Met Trp Lys Asn Asn Ser Gly Arg Pro Leu Gln Glu Thr Ala Pro 1040 1045 1050
- Phe Gly Cys Lys Ile Glu Val Glu Pro Leu Arg Ala Ser Asn Cys 1055 1060 1065
- Ala Tyr Gly His Ile Pro Ile Ser Ile Asp Ile Pro Asp Ala Ala Page 31

Phe Val Arg Ser Ser Glu Ser Pro Thr Ile Leu Glu Val Ser Cys 1085 1090 1095

Thr Val Ala Asp Cys Ile Tyr Ser Ala Asp Phe Gly Gly Ser Leu 1100 1105 1110

Thr Leu Gln Tyr Lys Ala Asp Arg Glu Gly His Cys Pro Val His 1115 1120 1125

Ser His Ser Thr Thr Ala Val Leu Lys Glu Ala Thr Thr His Val 1130 1140

Thr Ala Val Gly Ser Ile Thr Leu His Phe Ser Thr Ser Ser Pro 1145 1150 1155

Gln Ala Asn Phe Ile Val Ser Leu Cys Gly Lys Lys Ser Thr Cys 1160 1165 1170

Asn Ala Glu Cys Lys Pro Pro Ala Asp His Ile Ile Gly Glu Pro 1175 1180 1185

His Lys Val Asp Gln Glu Phe Gln Ala Ala Val Ser Lys Thr Ser 1190 1195 1200

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56; pcDW-XH7 nontranslated region 3857-4150

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cca aac cct cct agg cgc cgc tgg agg ccg ttt cgg ccc ccg ctg gct Pro Asn Pro Pro Arg Arg Arg Trp Arg Pro Phe Arg Pro Pro Leu Ala 25 30 35	272
gct caa atc gaa gat ctt agg agg tcg ata gtc aac ttg act ttc aaa Ala Gln Ile Glu Asp Leu Arg Arg Ser Ile Val Asn Leu Thr Phe Lys 40 45 50	320
caa cga tca cct aat ccg ccg cca ggt cca ccg cca aag aag aag Gln Arg Ser Pro Asn Pro Pro Pro Gly Pro Pro Pro Lys Lys Lys 55 60 65 70	368
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aag Lys 535	atg Met	aac Asn	ggc Gly	tgc Cys	act Thr 540	aaa Lys	gca Ala	aaa Lys	cag Gln	tgc Cys 545	att Ile	gcc Ala	tac Tyr	aag Lys	agc Ser 550	180	8
gac Asp	caa Gln	acg Thr	aaa Lys	tgg Trp 555	gtc Val	ttc Phe	aac Asn	tcg Ser	ccg Pro 560	gat Asp	ctt Leu	att Ile	agg Arg	cac His 565	aca Thr	185	6
gac Asp	cac His	tca Ser	gtg Val 570	caa Gln	ggt Gly	aaa Lys	ttg Leu	cac His 575	att Ile	cca Pro	ttc Phe	cgc Arg	ttg Leu 580	aca Thr	ccg Pro	190	4
					ccg Pro											, 195	2
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aca Thr 615	acg Thr	aga Arg	aaa Lys	ttg Leu	ggg Gly 620	ctg Leu	cga Arg	gca Ala	gac Asp	gca Ala 625	aca Thr	gca Ala	gaa Glu	tgg Trp	att Ile 630	204	8
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tgc Cys	ctg Leu	ggg Gly	aag Lys	gta Val 795	gac Asp	gcc Ala	ttc Phe	gaa Glu	cat His 800	gcg Ala	acc Thr	act Thr	gtg Val	cca Pro 805	aat Asn	25	76
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gcg Ala	tac Tyr	gtc Val 905	gag Glu	ttc Phe	gct Ala	cca Pro	gac Asp 910	tgc Cys	act Thr	ata Ile	gat Asp	сас ніs 915	gca Ala	gtc Val	gca Ala	29:	12
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	•	200				9:	9 0				99.)				
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	ccg Pro 1180					att Ile 1185									3737	7
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NEL-0001 Sequence Listing.txt Val Leu Val Cys Ser Ser Met Leu Ile Asn Thr Arg Arg 1225 1230 1235

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<211> 1236

<213> Western equine encephalomyelitis virus - strain 71V-1658

<400> 6

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Pro Met Ala Tyr Arg Asp Pro Asn Pro Pro Arg Arg Trp Arg Pro 20 25 30

Phe Arg Pro Pro Leu Ala Ala Gln Ile Glu Asp Leu Arg Arg Ser Ile 35 40 45

Val Asn Leu Thr Phe Lys Gln Arg Ser Pro Asn Pro Pro Pro Gly Pro 50 60

Pro Pro Lys Lys Lys Ser Ala Pro Lys Pro Lys Pro Thr Gln Pro 65 70 75 80

Lys Lys Lys Gln Gln Ala Lys Arg Thr Lys Arg Lys Pro Lys Pro 85 90 95

Gly Lys Arg Gln Arg Met Cys Met Lys Leu Glu Ser Asp Lys Thr Phe $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$

Pro Ile Met Leu Asn Gly Gln Val Asn Gly Tyr Ala Cys Val Val Gly 115 120 125

Gly Arg Leu Met Lys Pro Leu His Val Glu Gly Lys Ile Asp Asn Glu 130 135 140

Gln Leu Ala Ala Val Lys Leu Lys Lys Ala Ser Met Tyr Asp Leu Glu 145 150 155 160

Tyr Gly Asp Val Pro Gln Asn Met Lys Ser Asp Thr Leu Gln Tyr Thr 165 170 175 Page 38

Ser Asp Lys Pro Pro Gly Phe Tyr Asn Trp His His Gly Ala Val Gln 180 185 190 Tyr Glu Asn Gly Arg Phe Thr Val Pro Arg Gly Val Gly Gly Lys Gly 195 200 205 Asp Ser Gly Arg Pro Ile Leu Asp Asn Arg Gly Arg Val Val Ala Ile 210 215 220 Val Leu Gly Gly Ala Asn Glu Gly Thr Arg Thr Ala Leu Ser Val Val 225 230 235 Thr Trp Asn Gln Lys Gly Val Thr Ile Arg Asp Thr Pro Glu Gly Ser 245 250 255 Glu Pro Trp Ser Leu Val Thr Ala Leu Cys Val Leu Ser Asn Val Thr 260 265 270 Phe Pro Cys Asp Lys Pro Pro Val Cys Tyr Ser Leu Thr Pro Glu Arg 275 280 285 Thr Leu Asp Val Leu Glu Glu Asn Val Asp Asn Pro Asn Tyr Asp Thr 295 300 Leu Leu Glu Asn Val Leu Lys Cys Pro Ser Arg Arg Pro Lys Arg Ser 305 310 315 320 Ile Thr Asp Asp Phe Thr Leu Thr Ser Pro Tyr Leu Gly Phe Cys Pro 325 330 335 Tyr Cys Arg His Ser Thr Pro Cys Phe Ser Pro Ile Lys Ile Glu Asn 340 345 350 Val Trp Asp Glu Ser Asp Asp Gly Ser Ile Arg Ile Gln Val Ser Ala 355 360 365 Gln Phe Gly Tyr Asn Gln Ala Gly Thr Ala Asp Val Thr Lys Phe Arg 370 380 Tyr Met Ser Phe Asp His Asp His Asp Ile Lys Glu Asp Ser Met Glu 385 395 400 Lys Ile Ala Ile Ser Thr Ser Gly Pro Cys Arg Arg Leu Gly His Lys 405 410 415 Gly Tyr Phe Leu Leu Ala Gln Cys Pro Pro Gly Asp Ser Val Thr Val Page 39

Ser Ile Thr Ser Gly Ala Ser Glu Asn Ser Cys Thr Val Glu Lys Lys 435 440 445 Ile Arg Arg Lys Phe Val Gly Arg Glu Glu Tyr Leu Phe Pro Pro Val 450 455 460 His Gly Lys Leu Val Lys Cys His Val Tyr Asp His Leu Lys Glu Thr 465 470 475 480 Ser Ala Gly Tyr Ile Thr Met His Arg Pro Gly Pro His Ala Tyr Lys 485 490 495 Ser Tyr Leu Glu Glu Ala Ser Gly Glu Val Tyr Ile Lys Pro Pro Ser 500 505 510 Gly Lys Asn Val Thr Tyr Glu Cys Lys Cys Gly Asp Tyr Ser Thr Gly 515 520 525 Ile Val Ser Thr Arg Thr Lys Met Asn Gly Cys Thr Lys Ala Lys Gln 530 540 Cys Ile Ala Tyr Lys Ser Asp Gln Thr Lys Trp Val Phe Asn Ser Pro 545 550 560 Asp Leu Ile Arg His Thr Asp His Ser Val Gln Gly Lys Leu His Ile 565 570 575 Pro Phe Arg Leu Thr Pro Thr Val Cys Pro Val Pro Leu Ala His Thr 580 585 590 Pro Thr Val Thr Lys Trp Phe Lys Gly Ile Thr Leu His Leu Thr Ala 595 600 605 Met Arg Pro Thr Leu Leu Thr Thr Arg Lys Leu Gly Leu Arg Ala Asp 610 620 Ala Thr Ala Glu Trp Ile Thr Gly Ser Thr Ser Arg Asn Phe Ser Val Gly Arg Glu Gly Leu Glu Tyr Val Trp Gly Asn His Glu Pro Val Arg 645 650 655 Val Trp Ala Gln Glu Ser Ala Pro Gly Asp Pro His Gly Trp Pro His 660 665 670

NEL-0001 Sequence Listing.txt
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- Gly Leu Arg Ile Val Tyr Gly Asn Thr Thr Ala His Leu Asp Thr Phe 930 940
- Val Asn Gly Val Thr Pro Gly Ser Ser Arg Asp Leu Lys Val Ile Ala 945 950 955 960
- Gly Pro Ile Ser Ala Ala Phe Ser Pro Phe Asp His Lys Val Val Ile 965 970 975
- Arg Lys Gly Leu Val Tyr Asn Tyr Asp Phe Pro Glu Tyr Gly Ala Met 980 985 990
- Lys Pro Gly Ala Phe Gly Asp Ile Gln Ala Ser Ser Leu Asp Ala Thr 995 1000 1005
- Asp Ile Val Ala Arg Thr Asp Ile Arg Leu Leu Lys Pro Ser Val 1010 1015 1020
- Lys Asn Ile His Val Pro Tyr Thr Gln Ala Val Ser Gly Tyr Glu 1025 1030 1035
- Met Trp Lys Asn Asn Ser Gly Arg Pro Leu Gln Glu Thr Ala Pro 1040 1045 1050
- Phe Gly Cys Lys Ile Glu Val Glu Pro Leu Arg Ala Ser Asn Cys 1055 1060 1065
- Ala Tyr Gly His Ile Pro Ile Ser Ile Asp Ile Pro Asp Ala Ala 1070 1075 1080
- Phe Val Arg Ser Ser Glu Ser Pro Thr Ile Leu Glu Val Ser Cys 1085 1090 1095
- Thr Val Ala Asp Cys Ile Tyr Ser Ala Asp Phe Gly Gly Ser Leu 1100 11105 1110
- Thr Leu Gln Tyr Lys Ala Asp Arg Glu Gly His Cys Pro Val His 1115 1120 1125
- Ser His Ser Thr Thr Ala Val Leu Lys Glu Ala Thr Thr His Val 1130 1140
- Thr Ala Val Gly Ser Ile Thr Leu His Phe Ser Thr Ser Ser Pro 1145 1150 1155
- Gln Ala Asn Phe Ile Val Ser Leu Cys Gly Lys Lys Ser Thr Cys 1160 1165 1170 Page 42

Asn Ala Glu Cys Lys Pro Pro Ala Asp His Ile Ile Gly Glu Pro 1175 His Lys Val Asp Gln Glu Phe Gln Ala Ala Val Ser Lys Thr Ser 1200 1190 Phe Gly Gly Ala Ser Ser Leu Ile Trp Asn Trp Leu Leu Ala Leu 1215 1205 1210 Val Val Gly Leu Ile Val Leu Val Cys Ser Ser Met Leu Ile Asn 1220 1225 1230 Thr Arg Arg 1235 <210> 4395 <211> <212> DNA Western equine encephalomyelitis virus - STRAIN 71v-1658 <213> <220> CMV promoter <221> <222> (1)..(1260)Pvax vector sequence: 1-196; CMV promoter: 1-115; CMV putative tr anscriptional start site: 125; T7 promoter: 48-167; pvax multiclo ning region: 168-196; polyprotein (C-E3-E2-6K-E1): 214-4065; pcDW-HX45 nontranslated region: 4066-4348; pcDW-HX45 vector sequence: <223> 4349-4385; pVAX vector sequence: 4386 <400> 60 accaaaatca acgggacttt ccaaaatgtc gtaacaactc cgccccattg acgcaaatgg gcggtaggcg tgtacggtgg gaggtcatat ataagcagag tctctctggc taactagaga 120 180 acccactgct tactggctta tcgaaattaa tacgactcac tatagggaga cccaagctgg ctagcgttta aacttaagct tggtaccgag ctcatactgg caggcctgat catcacgtct 240 300 ctgtccacgt tagccgaaag cgttaagaac ttcaagagca taagagggag cccaatcacc ctctacggct gacctaaata ggtgacgtag tagacacgca cctacccacc gccagaatgt 360 420 ttccataccc tcagctgaac tttccaccag tttaccctac aaatccgatg gcttaccgag 480 atccaaaccc tcctaggcgc cgctggaggc cgtttcggcc cccgctggct gctcaaatcg 540 aagatcttag gaggtcgata gtcaacttga ctttcaaaca acgatcacct aatccgccgc 600 caggtccacc gccaaagaag aagaagagtg ctcctaagcc aaaacctact cagcctaaaa 660 agaagaagca qcaagccaag aggacgaaac gcaagcctaa accagggaaa cgacaacgta tgtgtatgaa gttggagtcg gacaagacat ttccgatcat gctgaacggc caagtgaatg 720 qatatqcctq cqttqtcqqa qqaaqqctqa tqaaaccact ccacqttqaa qqaaaaattg 780

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